

## AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** An isolated polynucleotide ~~selected from: (a) a~~ polynucleotide comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant, the sequence sharing at least 30% 95% sequence identity with the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof;

~~(b) a polynucleotide comprising a portion at least 300 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3 or of a complement of that sequence, wherein the portion encodes a polypeptide that confers disease resistance to a plant; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant and comprising the an amino acid sequence that shares at least 95% sequence identity with the sequence set forth in SEQ ID NO: 2 or 4; and (d) a polynucleotide comprising a nucleotide sequence that encodes a portion at least 100 contiguous amino acid residues in length of the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion at least 300 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant; (f) a polynucleotide comprising~~

(c) a nucleotide sequence that encodes a polypeptide that confers disease resistance to a plant, wherein the polynucleotide nucleotide sequence hybridises to the sequence of (a)[[L]] and (b), (e), (d), (e) or to a complement thereof, under at least low high stringency conditions; and (g) a polynucleotide comprising a portion at least 15 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3, or of a complement of that sequence, wherein the portion hybridises to a sequence of (a), (b), (e), (d), (e) or to a complement thereof, under at least low stringency conditions.

2. **(Original)** A nucleic acid construct, comprising a polynucleotide according to claim 1 operably connected to a regulatory element, which is operable in the plant.

3. (Original) A nucleic acid construct according to claim 2, wherein the construct is a vector.

4. (Original) An isolated host cell containing a nucleic acid construct according to claim 2.

5. (Original) A host cell according to claim 4, wherein the host cell is a plant cell.

6. (Original) A host cell according to claim 5, wherein the plant cell has the nucleic acid construct incorporated into its nucleome.

7. (Original) A host cell according to claim 5, wherein the plant cell has the nucleic acid construct stably incorporated into its genome.

8. (Original) A plant containing a cell comprising a nucleic acid construct according to claim 2.

9. (Original) A plant according to claim 8, wherein the plant cell has the nucleic acid construct stably incorporated into its genome.

10. (Canceled)

11. (Canceled)

12. (Canceled)

13. (Canceled)

14. (Currently amended) A method for modulating disease resistance in a plant, the method comprising introducing a construct into the nucleome of the plant and regenerating a stably transformed plant, the construct comprising a regulatory element operably connected to a polynucleotide nucleotide sequence selected from the group consisting of: (a) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant, the sequence sharing at least 30% 95% sequence identity with the sequence set forth in SEQ

ID NO: 1 or 3, or a complement thereof; (b) a polynucleotide comprising a portion at least 300 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3 or of a complement of that sequence, wherein the portion encodes a polypeptide that confers disease resistance to a plant; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant and comprising the an amino acid sequence that shares at least 95% sequence identity with the sequence set forth in SEQ ID NO: 2 or 4; (d) a polynucleotide comprising a nucleotide sequence that encodes a portion at least 100 contiguous amino acid residues in length of the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion at least 300 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant and (f) (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that confers disease resistance to a plant, wherein the polynucleotide nucleotide sequence hybridises to the sequence of (a)[L.] and (b), (c), (d), (e) or to a complement thereof, under at least low high stringency conditions.

15. (Original) A method according to claim 14, wherein the construct is introduced into regenerable plant cells so as to yield transformed plant cells.

16. (Original) A method according to claim 15, wherein the transformed plant cells are used for regenerating a differentiated plant.

17. (Original) A method according to claim 15, wherein the regenerable cells are regenerable dicotyledonous plant cells.

18. (Original) A method according to claim 15, wherein the regenerable cells are regenerable monocotyledonous plant cells.

19. (Original) A method according to claim 15, wherein regenerable cells are regenerable graminaceous monocotyledonous plant cells.

20. **(Original)** A method according to claim 15, wherein regenerable cells are regenerable non-graminaceous monocotyledonous plant cells.

21. **(Original)** A method according to claim 15, wherein regenerable cells are regenerable banana cells.

22. **(Original)** A method according to claim 16, wherein the expression of the polynucleotide renders the differentiated transgenic plant with enhanced resistance to disease.

23. **(Original)** A method according to claim 22, wherein disease is caused by a fungal pathogen.

24. **(Original)** A method according to claim 22, wherein disease is caused by soil borne fungi.

25. **(Original)** A method according to claim 22, wherein disease is caused by *Fusarium* species.

26. **(Original)** A method according to claim 16, wherein the nucleic acid construct is transmitted through a complete cycle of the differentiated transgenic plant to its progeny so that it is expressed by the progeny plants.

27. **(Original)** A method according to claim 26, wherein the progeny is selected from seed, plant parts, tissue, and progeny plants derived from the differentiated transgenic plant.

28. **(Currently amended)** A method of breeding a plant, the method comprising identifying a plant that is resistant to a pathogenic disease by detecting expression in the plant of a polynucleotide; and transferring from a the plant genetic material corresponding to a the polynucleotide via crossing and backcrossing to another plant, wherein the polynucleotide comprises a nucleotide sequence that is selected from the group consisting of: (a) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant, the sequence sharing at least 30% 95% sequence identity with the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof; (b) a polynucleotide comprising a portion at least 300

~~contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3 or of a complement of that sequence, wherein the portion encodes a polypeptide that confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant and comprising the an amino acid sequence that shares at least 95% sequence identity with the sequence set forth in SEQ ID NO: 2 or 4; (d) a polynucleotide comprising a nucleotide sequence that encodes a portion at least 100 contiguous amino acid residues in length of the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion at least 300 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant and (f) (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that confers disease resistance to a plant, wherein the polynucleotide nucleotide sequence hybridises to the sequence of (a)[[.]] or (b), (e), (d), (e) or to a complement thereof, under at least low high stringency conditions.~~

29. **(Original)** A method according to claim 28, wherein the other plant is susceptible to a pathogenic disease.

30. **(Original)** A method according to claim 29, wherein the disease is caused by a fungal pathogen.

31. **(Original)** A method according to claim 29, wherein the disease is caused by a *Fusarium* species.

32. **(Original)** A method according to claim 28, wherein the genetic material comprises naturally-occurring DNA.

33. **(Original)** A method according to claim 28, comprising: (1) sexually crossing a plant containing the genetic material with a plant from a pathogen susceptible taxon; (2) recovering reproductive material from the progeny of the cross; and (3) growing plants with enhanced resistance to the disease from the reproductive material.

34. (Canceled)

35. (Original) A method according to claim 33, further comprising repetitively: (a) backcrossing the disease resistant progeny with disease susceptible plants from the susceptible taxon; and (b) selecting for expression of a nucleic acid sequence corresponding to the polynucleotide or to marker gene associated with the polynucleotide among the progeny of the backcross, until the desired characteristics of the susceptible taxon are present in the progeny.

36. (Canceled)

37. (Canceled)

38. (Canceled)

39. (Canceled)

40. (Canceled)

41. (Canceled)

42. (Canceled)

43. (Canceled)

44. (Canceled)

45. (Canceled)

46. (Canceled)

47. (Currently amended) A polynucleotide comprising a nucleotide sequence encoding a polypeptide an amino acid sequence according to claim 37 selecting from the group consisting of  
(i) an amino acid sequence which confers disease resistance to a plant and which shares at least 95% sequence identity with the sequence set forth in SEQ ID NO: 2 or 4;

(ii) an amino acid sequence which confers disease resistance to a plant and which is encoded by a nucleotide sequence that shares at least 95% sequence identity with the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof;

(iii) an amino acid sequence which confers disease resistance to a plant and which is encoded by a nucleotide sequence that hybridises under high stringency conditions to the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof.

48. (Canceled)